

WEST Search History

[Hide Items](#) [Restore](#) [Clear](#) [Cancel](#)

DATE: Tuesday, December 07, 2004

Hide? Set Name Query **Hit Count**

DB=PGPB,USPT,EPAB; PLUR=YES; OP=ADJ

<input type="checkbox"/>	L25 L12 and L5	2
<input type="checkbox"/>	L24 L23 not @ay>1999	2
<input type="checkbox"/>	L23 L22 and L21	43
<input type="checkbox"/>	L22 cancer\$ or neoplas\$ or tumor\$ or metast\$	161041
<input type="checkbox"/>	L21 L20 and L5	43
<input type="checkbox"/>	L20 L16 and L1	210
<input type="checkbox"/>	L19 L18 and L5	5
<input type="checkbox"/>	L18 L17 and L16	11
<input type="checkbox"/>	L17 L1 and L15	12
<input type="checkbox"/>	L16 protective antigen	1339
<input type="checkbox"/>	L15 L14.in.	97
<input type="checkbox"/>	L14 leppla	226
<input type="checkbox"/>	L13 leppela	1
<input type="checkbox"/>	L12 L11 or L8 or L9 or L10	4
<input type="checkbox"/>	L11 5591631.pn.	1
<input type="checkbox"/>	L10 5817771.pn.	1
<input type="checkbox"/>	L9 5677274.pn.	1
<input type="checkbox"/>	L8 6468731.pn.	1
<input type="checkbox"/>	L7 L6 not @ay>1999	5
<input type="checkbox"/>	L6 L5 and L1	62
<input type="checkbox"/>	L5 plasminogen	14895
<input type="checkbox"/>	L4 L3 not @ay>1999	3
<input type="checkbox"/>	L3 L2 and plasminogen	57
<input type="checkbox"/>	L2 L1 and cancer	290
<input type="checkbox"/>	L1 lethal factor	382

END OF SEARCH HISTORY

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OM protein - protein search, using sw model

Run on: November 23, 2004, 12:21:54 ; Search time 116 Seconds
(without alignments)
522.631 Million cell updates/sec

Title: US-09-763-720-1
Perfect score: 870
Sequence: 1 GNEASYPLEMCSHFDADIEK.....EEFCAVVGGLDIHKKMVVVDV 169

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	Description

1	870	100.0	169	7	ADE55926	Ade55926 Rat Prote
2	870	100.0	169	7	ADE55928	Ade55928 Human Pro
3	870	100.0	170	2	AAW64200	Aaw64200 Human cal
4	870	100.0	170	3	AAB09978	Aab09978 Human HCN
5	870	100.0	170	8	ADI27357	Adi27357 Human cal
6	762	87.6	170	4	ABB60493	Abb60493 Drosophil
7	739	84.9	162	4	ABB65554	Abb65554 Drosophil
8	733	84.3	170	4	AAO14411	Aao14411 Calcineur
9	733	84.3	173	4	AAB64410	Aab64410 Amino aci

10	733	84.3	173	6	ADA55632		Ada55632	Human	pro
11	733	84.3	187	4	AAU87327		Aau87327	Novel	cen
12	733	84.3	187	8	ADI54642		Adi54642	Novel	hum
13	733	84.3	189	4	AAM95239		Aam95239	Human	rep
14	733	84.3	189	4	AAM43639		Aam43639	Human	pol
15	733	84.3	189	4	AAM43564		Aam43564	Human	pol
16	733	84.3	189	4	AAU19951		Aau19951	Novel	hum
17	733	84.3	189	4	ABB95936		Abb95936	Human	tes
18	733	84.3	189	4	AAU87615		Aau87615	Novel	cen
19	733	84.3	189	8	ADI54930		Adi54930	Novel	hum
20	733	84.3	189	8	ADM24660		Adm24660	Human	PRO
21	733	84.3	189	8	ADM24585		Adm24585	Human	PRO
22	728	83.7	170	3	AAB09977		Aab09977	Human	CNB
23	496	57.0	175	2	AAY00881		Aay00881	Calcineur	
24	393	45.2	90	3	AAG02990		Aag02990	Human	sec
25	373.5	42.9	178	3	AAY77951		Aay77951	A.	thalia
26	340.5	39.1	195	6	ABG74662		Abg74662	Murine	Ca
27	337.5	38.8	194	6	ABG74856		Abg74856	Human	cal
28	337.5	38.8	194	7	ADD46021		Add46021	Human	Pro
29	337.5	38.8	194	7	ADE59921		Ade59921	Human	Pro
30	337.5	38.8	194	7	ADE61228		Ade61228	Human	Pro
31	337.5	38.8	194	7	ADE59917		Ade59917	Human	Pro
32	337.5	38.8	195	6	ABG74661		Abg74661	Human	Ca2
33	337.5	38.8	195	6	ABU89717		Abu89717	Protein	d
34	321.5	37.0	189	4	ABB58936		Abb58936	Drosophil	
35	292	33.6	207	4	AAM43642		Aam43642	Human	pol
36	292	33.6	207	4	AAU19948		Aau19948	Novel	hum
37	292	33.6	207	4	AAU87620		Aau87620	Novel	cen
38	292	33.6	207	8	ADI54935		Adi54935	Novel	hum
39	292	33.6	207	8	ADM24663		Adm24663	Human	PRO
40	291	33.4	196	4	AAM78527		Aam78527	Human	pro
41	291	33.4	196	6	ABG74656		Abg74656	Human	Ca2
42	291	33.4	196	8	ADN04220		Adn04220	Antipsori	
43	291	33.4	210	4	AAU87336		Aau87336	Novel	cen
44	291	33.4	210	8	ADI54651		Adi54651	Novel	hum
45	289	33.2	199	4	ABB11947		Abb11947	Human	hep

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OM protein - nucleic search, using frame plus p2n model

Run on: November 23, 2004, 10:45:45 ; Search time 2592 Seconds
(without alignments)
3083.318 Million cell updates/sec

Title: US-09-763-720-1
Perfect score: 870
Sequence: 1 GNEASYPLEMCSHFDADIEK.....EEFCAVVGGLDIHKKMVVDV 169

Scoring table: BLOSUM62

Xgapop	10.0	,	Xgapext	0.5
Ygapop	10.0	,	Ygapext	0.5
Fgapop	6.0	,	Fgapext	7.0
Delop	6.0	,	Delext	7.0

Searched: 4526729 seqs, 23644849745 residues
 Total number of hits satisfying chosen parameters: 9053458
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries
 Command line parameters:
 -MODEL=frame+_p2n.model -DEV=xlp
 -
 Q=/cgn2_1/USPTO_spool_p/US09763720/runat_23112004_104537_3636/app_query.fasta_1.
 327
 -DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
 -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
 -USER=US09763720_@CGN_1_1_5600_@runat_23112004_104537_3636 -NCPU=6 -ICPU=3
 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
 -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:
 1: gb_ba:
 2: gb_htg:
 3: gb_in:
 4: gb_om:
 5: gb_ov:
 6: gb_pat:
 7: gb_ph:
 8: gb_pl:
 9: gb_pr:
 10: gb_ro:
 11: gb_sts:
 12: gb_sy:
 13: gb_un:
 14: gb_vi:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	870	100.0	513	9	CR456938	CR456938 Homo sapi
2	870	100.0	530	10	RATCALCB	L03554 Rattus norv
3	870	100.0	796	6	AX401980	AX401980 Sequence
4	870	100.0	796	10	RATRSCDPP	D14568 Rattus norv
5	870	100.0	840	6	AX827396	AX827396 Sequence
6	870	100.0	840	10	RATCALNB	D14425 Rat mRNA fo

7	870	100.0	841	4	BBCALCB	X71666	B.bovis	mRN	
8	870	100.0	1165	5	AY336970	AY336970	Gallus	ga	
9	870	100.0	1177	5	AY336972	AY336972	Xenopus	t	
10	870	100.0	1760	5	BC075185	BC075185	Xenopus	l	
11	870	100.0	2489	5	BC064854	BC064854	Xenopus	t	
12	870	100.0	2548	9	HUMCNR	M30773	Human	calci	
13	870	100.0	3112	9	BC027913	BC027913	Homo	sapi	
14	870	100.0	5498	6	BD270602	BD270602	Method	fo	
15	870	100.0	5525	6	BD270599	BD270599	Method	fo	
16	870	100.0	5528	6	BD270603	BD270603	Method	fo	
17	870	100.0	5555	6	BD270598	BD270598	Method	fo	
18	870	100.0	5557	6	BD270600	BD270600	Method	fo	
19	870	100.0	5611	6	BD270601	BD270601	Method	fo	
20	865	99.4	600	10	S43864	S43864	PP2B	beta 1	
21	860	98.9	861	5	AY336971	AY336971	Xenopus	l	
22	819	94.1	676	6	AX525920	AX525920	Sequence		
23	795	91.4	1551	10	AY266418	AY266418	Mus	muscu	
24	795	91.4	2298	9	AY183476	AY183476	Homo	sapi	
25	791	90.9	2043	3	AB041524	AB041524	Patinopec		
26	790	90.8	470	6	CQ719956	CQ719956	Sequence		
27	766	88.0	718	6	CQ595695	CQ595695	Sequence		
28	766	88.0	1085	3	BT003768	BT003768	Drosophil		
29	766	88.0	1157	3	AY089602	AY089602	Drosophil		
30	762	87.6	820	3	AF287251	AF287251	Bombyx	mo	
31	762	87.6	1174	3	DROCALCB	M97215	Drosophila		
32	762	87.6	1176	6	CQ580512	CQ580512	Sequence		
33	762	87.6	1235	3	AY070642	AY070642	Drosophil		
34	762	87.6	3176	6	CQ580511	CQ580511	Sequence		
c	35	762	87.6	27621	2	AC020338	AC020338	Drosophil	
c	36	762	87.6	167902	3	AC104604	AC104604	Drosophil	
37	762	87.6	170129	3	AC023712	AC023712	Drosophil		
38	762	87.6	303698	3	AE003434	AE003434	Drosophil		
39	749.5	86.1	222663	2	AC097549	AC097549	Rattus	no	
40	734.5	84.4	1266	3	AY220751	AY220751	Schistoso		
41	733	84.3	510	6	AX259269	AX259269	Sequence		
42	733	84.3	851	9	AF145026	AF145026	Homo	sapi	
43	733	84.3	879	6	AX058224	AX058224	Sequence		
44	733	84.3	905	9	AF400667	AF400667	Homo	sapi	
45	733	84.3	1035	9	BC066299	BC066299	Homo	sapi	

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OM protein - nucleic search, using frame plus p2n model

Run on: November 23, 2004, 10:45:45 ; Search time 389 Seconds
(without alignments)
2280.597 Million cell updates/sec

Title: US-09-763-720-1

Perfect score: 870

Sequence: 1 GNEASYPLEMCSHFDADEIK.....EEFCAVVGGLDIHKMVKVVDV 169

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp

-Q=/cgn2_1/USPTO_spool_p/US09763720/runat_23112004_104537_3629/app_query.fasta_1.
327
-DB=N_Geneseq_23Sep04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09763720_@CGN_1_1_708_@runat_23112004_104537_3629 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_23Sep04:
1: geneseqn1980s:
2: geneseqn1990s:
3: geneseqn2000s:
4: geneseqn2001as:
5: geneseqn2001bs:
6: geneseqn2002as:
7: geneseqn2002bs:
8: geneseqn2003as:
9: geneseqn2003bs:
10: geneseqn2003cs:
11: geneseqn2003ds:
12: geneseqn2004s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB ID	
<hr/>						
1	870	100.0	796	6	ABK63749	Abk63749 Rat seque
2	870	100.0	796	10	ADB52863	Adb52863 Primary r
3	870	100.0	2548	12	ADI27256	Adi27256 Human cDN
4	819	94.1	676	6	ABT09354	Abt09354 Phase-1 R
5	819	94.1	676	12	ADH22712	Adh22712 Partial D

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OM protein - protein search, using sw model

Run on: November 23, 2004, 13:34:48 ; Search time 40 Seconds
(without alignments)
406.516 Million cell updates/sec

Title: US-09-763-720-1
Perfect score: 870
Sequence: 1 GNEASYPLEMCSHFDADEIK.....EEFCAVVGGLDIHKKMVVDV 169

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Query Score	Match	Length	DB	ID	Description
1	870	100.0	170	1	A33391	calcineurin regula
2	870	100.0	170	1	S34127	calcineurin regula
3	870	100.0	216	1	S42716	calcineurin regula
4	865	99.4	170	1	JC1220	calcineurin regula
5	784	90.1	170	2	JC7242	calcineurin regula
6	766	88.0	170	2	JC5174	calcineurin regula
7	762	87.6	170	2	A44307	calcineurin regula
8	704	80.9	369	2	T22708	hypothetical prote
9	702	80.7	179	2	JC1221	calcineurin regula
10	699	80.3	176	2	JQ1232	calcineurin regula
11	620	71.3	165	2	PS0261	calcineurin regula
12	528	60.7	174	2	T47245	calcineurin regula
13	496	57.0	175	2	JH0462	phosphoprotein pho
14	483	55.5	174	2	T41632	probable calcineur
15	316.5	36.4	213	2	T31775	hypothetical prote
16	303.5	34.9	195	2	T28047	hypothetical prote
17	255	29.3	311	2	T21563	hypothetical prote
18	233.5	26.8	150	2	T07122	calmodulin CAM5 -
19	233.5	26.8	151	2	A71409	calmodulin 8 [impo
20	230	26.4	591	2	S54788	calcium-stimulated
21	229.5	26.4	149	2	S35187	calmodulin 6 - Ara
22	228.5	26.3	149	1	S53006	calmodulin - leaf
23	228.5	26.3	149	1	MCPZDC	calmodulin - carro
24	228.5	26.3	149	1	S22503	calmodulin [simila
25	228.5	26.3	149	1	S22971	calmodulin - trump
26	228.5	26.3	149	1	S40301	calmodulin - red b
27	228.5	26.3	149	1	S70768	calmodulin CAM81 -
28	228.5	26.3	149	2	T47417	calmodulin 7 [simi
29	228.5	26.3	149	2	H84667	calmodulin (cam2)

30	227.5	26.1	149	1	MCBH	calmodulin - barle
31	227.5	26.1	149	1	MCWT	calmodulin - wheat
32	227.5	26.1	149	2	S24952	calmodulin 1 (clon
33	226.5	26.0	149	2	S58311	calmodulin - Biden
34	226.5	26.0	149	2	S60237	calmodulin PCM2/PC
35	225.5	25.9	149	1	MCZQF	calmodulin - malar
36	224.5	25.8	149	1	MCAA	calmodulin - alfal
37	224.5	25.8	149	2	S22860	calmodulin 2 (clon
38	223.5	25.7	149	1	I51202	calmodulin - duck
39	223.5	25.7	149	1	MCCH	calmodulin - chick
40	223.5	25.7	149	1	MCEE	calmodulin - elect
41	223.5	25.7	149	1	MCHU	calmodulin [valida
42	223.5	25.7	149	1	MCRT	calmodulin [valida
43	223.5	25.7	149	2	JC1305	calmodulin - Japan
44	223.5	25.7	149	2	I51402	calmodulin - Afric
45	223.5	25.7	149	2	S37707	calmodulin - mouse

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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 23, 2004, 10:45:45 ; Search time 3034 Seconds
(without alignments)
2029.768 Million cell updates/sec

Title: US-09-763-720-1
Perfect score: 870
Sequence: 1 GNEASYPLEMCSHFDADIEK.....EEFCAVVGGLDIHKKMVVDV 169

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp

- Q=/cgn2_1/USPTO_spool_p/US09763720/runat_23112004_104538_3648/app_query.fasta_1.
327

-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL

-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
 -USER=US09763720_@CGN_1_1_5180_@runat_23112004_104538_3648 -NCPU=6 -ICPU=3
 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
 -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_htc:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_gss1:*
- 9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
1	870	100.0	543	5	BQ617594	BQ617594 faa65d11.
2	870	100.0	632	5	BQ396782	BQ396782 NISC_ng22
3	870	100.0	694	1	AJ449933	AJ449933 AJ449933
4	870	100.0	704	5	BX852145	BX852145 BX852145
5	870	100.0	725	5	BX731180	BX731180 BX731180
6	870	100.0	732	7	CK694046	CK694046 ZF101-P00
7	870	100.0	744	4	BJ069874	BJ069874 BJ069874
8	870	100.0	785	7	CR409344	CR409344 CR409344
9	870	100.0	787	7	CK309466	CK309466 SB02049B1
10	870	100.0	788	7	CF999354	CF999354 AGENCOURT
11	870	100.0	793	6	CA320261	CA320261 UI-M-FW0-
12	870	100.0	806	7	CK024626	CK024626 AGENCOURT
13	870	100.0	862	6	CD358564	CD358564 AGENCOURT
14	870	100.0	874	7	CR415089	CR415089 CR415089
15	870	100.0	941	7	CK697326	CK697326 ZF101-P00
16	870	100.0	1015	7	CN062381	CN062381 Ag2_p36_J
17	870	100.0	1352	3	CR719704	CR719704 Tetraodon
18	866	99.5	754	6	CA320149	CA320149 UI-M-FW0-
19	864	99.3	557	4	BG511941	BG511941 dad30d10.
20	864	99.3	598	4	BG159744	BG159744 de68a05.y
21	863	99.2	884	7	CO771498	CO771498 testis_ES
22	860	98.9	801	5	BX876992	BX876992 BX876992
23	860	98.9	815	7	CR409418	CR409418 CR409418
24	860	98.9	861	6	CA793813	CA793813 AGENCOURT
25	859	98.7	577	7	CN677314	CN677314 A0994E09-
26	859	98.7	1275	3	CR664353	CR664353 Tetraodon
27	859	98.7	1384	3	CR685150	CR685150 Tetraodon
28	857	98.5	641	4	BJ068201	BJ068201 BJ068201
29	857	98.5	810	7	CN226007	CN226007 WLA082F10
30	854	98.2	846	1	AL528885	AL528885 AL528885
31	851	97.8	692	1	AJ453031	AJ453031 AJ453031

32	850	97.7	666	1	AL848613	AL848613
33	850	97.7	790	6	CA315198	UI-M-FW0-
34	846	97.2	1283	3	CR675015	Tetraodon
35	844	97.0	647	1	AL650076	AL650076
36	844	97.0	690	5	BX485177	BX485177 DKFZp686B
37	844	97.0	892	7	CR583442	CR583442
38	841	96.7	681	4	BI850954	BI850954 imageqc_1
39	839	96.4	684	1	AJ448377	AJ448377
40	830	95.4	693	7	CF737405	CF737405 UI-M-HD0-
41	829	95.3	668	7	CN088515	CN088515 EC2BBA30A
42	827	95.1	718	7	CN527485	CN527485 UI-M-HQ0-
43	826	94.9	701	4	BI394649	BI394649 pgpln.pk0
44	824	94.7	594	4	BI476144	BI476144 fp52h05.y
45	824	94.7	882	5	BX702992	BX702992 BX702992

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OM protein - protein search, using sw model

Run on: November 23, 2004, 13:28:03 ; Search time 131 Seconds
(without alignments)
742.277 Million cell updates/sec

Title: US-09-763-720-1
Perfect score: 870
Sequence: 1 GNEASYPLEMCSHFDADAEIK.....EEFCAVVGGLDIHKKMVVVDV 169

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:
1: uniprot_sprot:
2: uniprot_trembl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB	ID	%	Description
					%	

1	870	100.0	169	1	CALB_HUMAN	P06705 homo sapien
2	870	100.0	170	2	Q6VN50	Q6vn50 xenopus tro
3	870	100.0	170	2	Q6VN51	Q6vn51 gallus gall
4	870	100.0	170	2	Q6DJJ3	Q6djj3 xenopus lae
5	870	100.0	170	2	AAQ16146	Aaq16146 gallus ga
6	870	100.0	170	2	AAQ16148	Aaq16148 xenopus t
7	870	100.0	170	2	AAH64854	Aah64854 xenopus t
8	870	100.0	170	2	CAG33219	Cag33219 homo sapi
9	865	99.4	169	1	CALB_MOUSE	Q63810 mus musculu
10	860	98.9	170	2	Q7T063	Q7t063 xenopus lae
11	795	91.4	765	2	Q86YQ0	Q86yq0 homo sapien
12	791	90.9	170	2	Q9NWK7	Q9nk7 patinopecte
13	769	88.4	169	2	Q7PQ91	Q7pq91 anopheles g
14	766	88.0	170	1	CALC_DROME	Q24214 drosophila
15	762	87.6	170	1	CALB_DROME	P48451 drosophila
16	762	87.6	170	2	Q95P81	Q95p81 bombyx mori
17	734.5	84.4	169	2	Q86H16	Q86h16 schistosoma
18	733	84.3	170	2	Q7Z4V8	Q7z4v8 homo sapien
19	733	84.3	173	2	Q96LZ3	Q96l73 homo sapien
20	733	84.3	173	2	AAH66299	Aah66299 homo sapi
21	732.5	84.2	169	2	Q9NFn1	Q9nfn1 schistosoma
22	728	83.7	170	2	Q8WYJ4	Q8wyj4 homo sapien
23	707	81.3	170	2	Q7YRC9	Q7yrc9 macaca mula
24	704	80.9	171	2	Q20804	Q20804 caenorhabdi
25	702	80.7	178	1	CALC_MOUSE	Q63811 mus musculu
26	702	80.7	179	2	BAC26725	Bac26725 mus muscu
27	699	80.3	175	1	CALC_RAT	P28470 rattus norv
28	580	66.7	115	2	Q99LQ9	Q99lq9 mus musculu
29	544	62.5	173	2	Q6CGE6	Q6cge6 yarrowia li
30	528	60.7	174	1	CALB_NEUCR	P87072 neurospora
31	528	60.7	175	2	Q9HDE1	Q9hde1 cryptococcu
32	517	59.4	177	1	CALB_NAEGR	P42322 naegleria g
33	517	59.4	177	2	Q9HDD3	Q9hdd3 cryptococcu
34	499	57.4	175	2	Q757B7	Q757b7 ashbya goss
35	499	57.4	175	2	AAS52780	Aas52780 ashbya go
36	496	57.0	174	1	CALB YEAST	P25296 saccharomyc
37	483	55.5	174	1	CALB_SCHPO	Q9uu93 schizosacch
38	483	55.5	175	2	Q6FLU4	Q6flu4 candida gla
39	477.5	54.9	215	2	Q7S748	Q7s748 neurospora
40	475	54.6	175	2	Q874T7	Q874t7 kluyveromyc
41	469	53.9	174	2	Q6BWS8	Q6bws8 debaryomyce
42	451	51.8	177	2	Q8MQT6	Q8mqt6 toxoplasma
43	443.5	51.0	169	2	Q867N3	Q867n3 paramecium
44	442.5	50.9	180	2	Q9GP83	Q9gp83 dictyosteli
45	436	50.1	177	2	Q86RA7	Q86ra7 plasmodium